

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lin, Lih-Ling
Graham, James
- (ii) TITLE OF INVENTION: NOVEL INTERLEUKIN-1 RECEPTOR
INTRACELLULAR LIGAND PROTEINS AND INHIBITORS OF LIGAND
BINDING
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LEGAL AFFAIRS, GENETICS INSTITUTE, INC.
 - (B) STREET: 87 CambridgePark Drive
 - (C) CITY: Cambridge
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02140
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Brown, Scott A.
 - (B) REGISTRATION NUMBER: 32,724
 - (C) REFERENCE/DOCKET NUMBER: GI5258
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 498-8224
 - (B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1571 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 2..529
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

G ATC CCC AGG GTG GAC CTC CGG GTG TGG CAG GAC TGC TGT GAA GAC
 Ile Pro Arg Val Asp Leu Arg Val Trp Gln Asp Cys Cys Glu Asp
 1 5 10 15

46

[illegible]

GAAACAGGTT TGCTTTCAGC TGCTCACTGC ACACATACTG CCTAGTTGTG AACCAAATGT 1359
 GAAAAAACCT CCTTCATCCC ATTGTGTATC TGATACCTGC CGAGGGCCAA GGGTGTGTGT 1419
 TGACAACGCC GCTCCCAGCC GGCCCTGGTT GCGTCCACGT CCTGAACAAG AGCCGCTTCC 1479
 GGATGGCTCT TCCCAAGGGA GGAGGAGCTC AAGTGTCTGG AACTGTCTAA CTTCAGGTTG 1539
 TGTGAGTGCG TTAATAAAAAA AAAAAAAA AA 1571

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Pro Arg Val Asp Leu Arg Val Trp Gln Asp Cys Cys Glu Asp Cys
 1 5 10 15
 Arg Thr Arg Gly Gln Phe Asn Ala Phe Ser Tyr His Phe Arg Gly Arg
 20 25 30
 Arg Ser Leu Glu Phe Ser Tyr Gln Glu Asp Lys Pro Thr Lys Lys Thr
 35 40 45
 Arg Pro Arg Lys Ile Pro Ser Val Gly Arg Gln Gly Glu His Leu Ser
 50 55 60
 Asn Ser Thr Ser Ala Phe Ser Thr Arg Ser Asp Ala Ser Gly Thr Asn
 65 70 75 80
 Asp Phe Arg Glu Phe Val Leu Glu Met Gln Lys Thr Ile Thr Asp Leu
 85 90 95
 Arg Thr Gln Ile Lys Lys Leu Glu Ser Arg Leu Ser Thr Thr Glu Cys
 100 105 110
 Val Asp Ala Gly Gly Glu Ser His Ala Asn Asn Thr Lys Trp Lys Lys
 115 120 125
 Asp Ala Cys Thr Ile Cys Glu Cys Lys Asp Gly Gln Val Thr Cys Phe
 130 135 140
 Val Glu Ala Cys Pro Pro Ala Thr Cys Ala Val Pro Val Asn Ile Pro
 145 150 155 160
 Gly Ala Cys Cys Pro Val Cys Leu Gln Lys Arg Ala Glu Glu Lys Pro
 165 170 175

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1088 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 2..961

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

G AAA AAA GGA GGT AAA ACA GAA CAG GAT GGC TAT CAG AAA CCC ACC	46
Lys Lys Gly Gly Lys Thr Glu Gln Asp Gly Tyr Gln Lys Pro Thr	
1 5 10 15	
AAC AAA CAC TTC ACG CAG AGT CCC AAG AAG TCA GTG GCC GAC CTG CTG	94
Asn Lys His Phe Thr Gln Ser Pro Lys Lys Ser Val Ala Asp Leu Leu	
20 25 30	
GGG TCC TTT GAA GGC AAA CGA AGA CTC CTT CTG ATC ACT GCT CCC AAG	142
Gly Ser Phe Glu Gly Lys Arg Arg Leu Leu Leu Ile Thr Ala Pro Lys	
35 40 45	
GCT GAG AAC AAT ATG TAT GTG CAA CAA CGT GAT GAA TAT CTG GAA AGT	190
Ala Glu Asn Asn Met Tyr Val Gln Gln Arg Asp Glu Tyr Leu Glu Ser	
50 55 60	
TTC TGC AAG ATG GCT ACC AGG AAA ATC TCT GTG ATC ACC ATC TTC GGC	238
Phe Cys Lys Met Ala Thr Arg Lys Ile Ser Val Ile Thr Ile Phe Gly	
65 70 75	
CCT GTC AAC AAC AGC ACC ATG AAA ATC GAC CAC TTT CAG CTA GAT AAT	286
Pro Val Asn Asn Ser Thr Met Lys Ile Asp His Phe Gln Leu Asp Asn	
80 85 90 95	
GAG AAG CCC ATG CGA GTG GTG GAT GAT GAA GAC TTG GTA GAC CAG CGT	334
Glu Lys Pro Met Arg Val Val Asp Asp Glu Asp Leu Val Asp Gln Arg	
100 105 110	
CTC ATC AGC GAG CTG AGG AAA GAG TAC GGA ATG ACC TAC AAT GAC TTC	382
Leu Ile Ser Glu Leu Arg Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe	
115 120 125	
TTC ATG GTG CTA ACA GAT GTG GAT CTG AGA GTC AAG CAA TAC TAT GAG	430
Phe Met Val Leu Thr Asp Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu	
130 135 140	
GTA CCA ATA ACA ATG AAG TCT GTG TTT GAT CTG ATC GAT ACT TTC CAG	478
Val Pro Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln	
145 150 155	
TCC CGA ATC AAA GAT ATG GAG AAG CAG AAG AAG GAG GGC ATT GTT TGC	526
Ser Arg Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys	
160 165 170 175	
AAA GAG GAA GTT GGG GGA GTG TTA GAA CTG TTC CCA ATT AAT GGG AGC	574
Lys Glu Glu Val Gly Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser	
180 185 190	
TCT GTT GTT GAG CGA GAA GAC GTA CCA GCC CAT TTG GTG AAA GAC ATT	622
Ser Val Val Glu Arg Glu Asp Val Pro Ala His Leu Val Lys Asp Ile	
195 200 205	
CGT AAC TAT TTT CAA GTG AGC CCG GAG TAC TTC TCC ATG CTT CTA GTC	670
Arg Asn Tyr Phe Gln Val Ser Pro Glu Tyr Phe Ser Met Leu Leu Val	
210 215 220	
GGA AAA GAC GGA AAT GTC AAA TCC TGG TAT CCT TCC CCA ATG TGG TCC	718
Gly Lys Asp Gly Asn Val Lys Ser Trp Tyr Pro Ser Pro Met Trp Ser	
225 230 235	

ATG GTG ATT GTG TAC GAT TTA ATT GAT TCG ATG CAA CTT CGG AGA CAG	766
Met Val Ile Val Tyr Asp Leu Ile Asp Ser Met Gln Leu Arg Arg Gln	
240 245 250 255	
GAA ATG GCG ATT CAG CAG TCA CTG GGG ATG CGC TGC CAG AAG ATG AGT	814
Glu Met Ala Ile Gln Gln Ser Leu Gly Met Arg Cys Gln Lys Met Ser	
260 265 270	
ATG CAG GCT ATG GTT ACC ATA GTT ACC ACC AAG GAT ACC AGG ATG GTT	862
Met Gln Ala Met Val Thr Ile Val Thr Thr Lys Asp Thr Arg Met Val	
275 280 285	
ACC AGG ATG ACT ACC GTC ATC ATG AGA GTT ATC ACC ATG GAT ACC CTT	910
Thr Arg Met Thr Thr Val Ile Met Arg Val Ile Thr Met Asp Thr Leu	
290 295 300	
ACT GAG CAG AAA TAT GTA ACC TTA GAC TCA GCC AGT TTC CTC TGC AGC	958
Thr Glu Gln Lys Tyr Val Thr Leu Asp Ser Ala Ser Phe Leu Cys Ser	
305 310 315	
TGC TAAAACTACA TGTGGCCAGC TCCATTCTTC CACACTGCGT ACTACATTTT	1011
Cys	
320	
CTGCCTTTTT CTTCAGTGT TTTTCTAAGA CTAAATAAAT AGCAAACCTTT CACCTAAAAA	1071
AAAAAAAAAA AAAAAA	1088

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Lys	Lys	Gly	Gly	Lys	Thr	Glu	Gln	Asp	Gly	Tyr	Gln	Lys	Pro	Thr	Asn
1				5					10					15	
Lys	His	Phe	Thr	Gln	Ser	Pro	Lys	Lys	Ser	Val	Ala	Asp	Leu	Leu	Gly
			20					25					30		
Ser	Phe	Glu	Gly	Lys	Arg	Arg	Leu	Leu	Leu	Ile	Thr	Ala	Pro	Lys	Ala
		35					40					45			
Glu	Asn	Asn	Met	Tyr	Val	Gln	Gln	Arg	Asp	Glu	Tyr	Leu	Glu	Ser	Phe
	50					55				60					
Cys	Lys	Met	Ala	Thr	Arg	Lys	Ile	Ser	Val	Ile	Thr	Ile	Phe	Gly	Pro
	65				70					75					80
Val	Asn	Asn	Ser	Thr	Met	Lys	Ile	Asp	His	Phe	Gln	Leu	Asp	Asn	Glu
			85						90					95	
Lys	Pro	Met	Arg	Val	Val	Asp	Asp	Glu	Asp	Leu	Val	Asp	Gln	Arg	Leu
			100					105					110		
Ile	Ser	Glu	Leu	Arg	Lys	Glu	Tyr	Gly	Met	Thr	Tyr	Asn	Asp	Phe	Phe
		115					120					125			
Met	Val	Leu	Thr	Asp	Val	Asp	Leu	Arg	Val	Lys	Gln	Tyr	Tyr	Glu	Val
		130				135					140				

Pro Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln Ser
 145 150 155 160
 Arg Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys Lys
 165 170 175
 Glu Glu Val Gly Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser Ser
 180 185 190
 Val Val Glu Arg Glu Asp Val Pro Ala His Leu Val Lys Asp Ile Arg
 195 200 205
 Asn Tyr Phe Gln Val Ser Pro Glu Tyr Phe Ser Met Leu Leu Val Gly
 210 215 220
 Lys Asp Gly Asn Val Lys Ser Trp Tyr Pro Ser Pro Met Trp Ser Met
 225 230 235 240
 Val Ile Val Tyr Asp Leu Ile Asp Ser Met Gln Leu Arg Arg Gln Glu
 245 250 255
 Met Ala Ile Gln Gln Ser Leu Gly Met Arg Cys Gln Lys Met Ser Met
 260 265 270
 Gln Ala Met Val Thr Ile Val Thr Thr Lys Asp Thr Arg Met Val Thr
 275 280 285
 Arg Met Thr Thr Val Ile Met Arg Val Ile Thr Met Asp Thr Leu Thr
 290 295 300
 Glu Gln Lys Tyr Val Thr Leu Asp Ser Ala Ser Phe Leu Cys Ser Cys
 305 310 315 320

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1759 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 2..754

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

C AAA AAC TTC TTC CTG ACG AAT CGC GCC AGG GAG CGC TCA GAC ACC	46
Lys Asn Phe Phe Leu Thr Asn Arg Ala Arg Glu Arg Ser Asp Thr	
1 5 10 15	
TTC ATC AAC CTC CGG GAG GTG CTC AAC CGC TTC AAG CTG CCG CCA GGA	94
Phe Ile Asn Leu Arg Glu Val Leu Asn Arg Phe Lys Leu Pro Pro Gly	
20 25 30	
GAG TAC ATT CTC GTG CCT TCC ACC TTC GAA CCC AAC AAG GAT GGG GAT	142
Glu Tyr Ile Leu Val Pro Ser Thr Phe Glu Pro Asn Lys Asp Gly Asp	
35 40 45	

TTC	TGC	ATC	CGG	GTC	TTT	TCT	GAA	AAG	AAA	GCT	GAC	TAC	CAA	GCT	GTC		190
Phe	Cys	Ile	Arg	Val	Phe	Ser	Glu	Lys	Lys	Ala	Asp	Tyr	Gln	Ala	Val		
		50						55					60				
GAT	GAT	GAA	ATC	GAG	GCC	AAT	CTT	GAA	GAG	TTC	GAC	ATC	AGC	GAG	GAT		238
Asp	Asp	Glu	Ile	Glu	Ala	Asn	Leu	Glu	Glu	Phe	Asp	Ile	Ser	Glu	Asp		
		65				70					75						
GAC	ATT	GAT	GAT	GGA	TTC	AGG	AGA	CTG	TTT	GCC	CAG	TTG	GCA	GGA	GAG		286
Asp	Ile	Asp	Asp	Gly	Phe	Arg	Arg	Leu	Phe	Ala	Gln	Leu	Ala	Gly	Glu		
					85					90					95		
GAT	GCG	GAG	ATC	TCT	GCC	TTT	GAG	CTG	CAG	ACC	ATC	CTG	AGA	AGG	GTT		334
Asp	Ala	Glu	Ile	Ser	Ala	Phe	Glu	Leu	Gln	Thr	Ile	Leu	Arg	Arg	Val		
				100					105					110			
CTA	GCA	AAG	CGC	CAA	GAT	ATC	AAG	TCA	GAT	GGC	TTC	AGC	ATC	GAG	ACA		382
Leu	Ala	Lys	Arg	Gln	Asp	Ile	Lys	Ser	Asp	Gly	Phe	Ser	Ile	Glu	Thr		
			115					120					125				
TGC	AAA	ATT	ATG	GTT	GAC	ATG	CTA	GAT	TCG	GAC	GGG	AGT	GGC	AAG	CTG		430
Cys	Lys	Ile	Met	Val	Asp	Met	Leu	Asp	Ser	Asp	Gly	Ser	Gly	Lys	Leu		
		130					135					140					
GGG	CTG	AAG	GAG	TTC	TAC	ATT	CTC	TGG	ACG	AAG	ATT	CAA	AAA	TAC	CAA		478
Gly	Leu	Lys	Glu	Phe	Tyr	Ile	Leu	Trp	Thr	Lys	Ile	Gln	Lys	Tyr	Gln		
		145				150					155						
AAA	ATT	TAC	CGA	GAA	ATC	GAC	GTT	GAC	AGG	TCT	GGT	ACC	ATG	AAT	TCC		526
Lys	Ile	Tyr	Arg	Glu	Ile	Asp	Val	Asp	Arg	Ser	Gly	Thr	Met	Asn	Ser		
					165				170						175		
TAT	GAA	ATG	CGG	AAG	GCA	TTA	GAA	GAA	GCA	GGT	TTC	AAG	ATG	CCC	TGT		574
Tyr	Glu	Met	Arg	Lys	Ala	Leu	Glu	Glu	Ala	Gly	Phe	Lys	Met	Pro	Cys		
				180					185					190			
CAA	CTC	CAC	CAA	GTC	ATC	GTT	GCT	CGG	TTT	GCA	GAT	GAC	CAG	CTC	ATC		622
Gln	Leu	His	Gln	Val	Ile	Val	Ala	Arg	Phe	Ala	Asp	Asp	Gln	Leu	Ile		
			195					200					205				
ATC	GAT	TTT	GAT	AAT	TTT	GTT	CGG	TGT	TTG	GTT	CGG	CTG	GAA	ACG	CTA		670
Ile	Asp	Phe	Asp	Asn	Phe	Val	Arg	Cys	Leu	Val	Arg	Leu	Glu	Thr	Leu		
		210					215					220					
TTC	AAG	ATA	TTT	AAG	CAG	CTG	GAT	CCC	GAG	AAT	ACT	GGA	ACA	ATA	GAG		718
Phe	Lys	Ile	Phe	Lys	Gln	Leu	Asp	Pro	Glu	Asn	Thr	Gly	Thr	Ile	Glu		
		225				230					235						
CTC	GAC	CTT	ATC	TCT	TGG	CTC	TGT	TTC	TCA	GTA	CTT	TGAAGTTATA					764
Leu	Asp	Leu	Ile	Ser	Trp	Leu	Cys	Phe	Ser	Val	Leu						
					245</												

GGAAACATGG TATATCATGA AGTAATCTTG TCAAGGCATC TGGAGAGTCC AGGAGAGAAG 1304
 ACTCACCTCT GTCGCTTGGG TTAAACAAGA GACAGGTTTT GTAGAATATT GATTGGTAAT 1364
 AGTAAATCGT TCTCCTTACA ATCAAGTTCT TGACCCTATT CGGCCTTATA CATCTGGTCT 1424
 TACAAAGACC AAAGGGATCC TGCCTTGAT CAACTGAACC AGTATGCCAA AACCAGGCAT 1484
 CCAATTTGTA AACCAATTAT GATAAAGGAC AAAATAAGCT GTTTGCCACC TCAAACTTT 1544
 ATGAACTTCA CCACCACTAG TGTCTGTCCA TGGAGTTAGA GGGGACATCA CTTAGAAGTT 1604
 CTTATAGAAA GGACACAAGT TTGTTTCCTG GCTTTACCTT GGGAAAATGC TAGCAACATT 1664
 ATAGAAATTT TGCCTTGTTG CCTTATCTTC TTCCAAATGT ACTGTAAAT AAAAATAAAG 1724
 GGTTACCCCA TGCAATCAAA AAAAAAAAAA AAAAA 1759

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Lys Asn Phe Phe Leu Thr Asn Arg Ala Arg Glu Arg Ser Asp Thr Phe
 1 5 10 15
 Ile Asn Leu Arg Glu Val Leu Asn Arg Phe Lys Leu Pro Pro Gly Glu
 20 25 30
 Tyr Ile Leu Val Pro Ser Thr Phe Glu Pro Asn Lys Asp Gly Asp Phe
 35 40 45
 Cys Ile Arg Val Phe Ser Glu Lys Lys Ala Asp Tyr Gln Ala Val Asp
 50 55 60
 Asp Glu Ile Glu Ala Asn Leu Glu Glu Phe Asp Ile Ser Glu Asp Asp
 65 70 75 80
 Ile Asp Asp Gly Phe Arg Arg Leu Phe Ala Gln Leu Ala Gly Glu Asp
 85 90 95
 Ala Glu Ile Ser Ala Phe Glu Leu Gln Thr Ile Leu Arg Arg Val Leu
 100 105 110
 Ala Lys Arg Gln Asp Ile Lys Ser Asp Gly Phe Ser Ile Glu Thr Cys
 115 120 125
 Lys Ile Met Val Asp Met Leu Asp Ser Asp Gly Ser Gly Lys Leu Gly
 130 135 140
 Leu Lys Glu Phe Tyr Ile Leu Trp Thr Lys Ile Gln Lys Tyr Gln Lys
 145 150 155 160
 Ile Tyr Arg Glu Ile Asp Val Asp Arg Ser Gly Thr Met Asn Ser Tyr
 165 170 175
 Glu Met Arg Lys Ala Leu Glu Glu Ala Gly Phe Lys Met Pro Cys Gln
 180 185 190

[illegible]

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

Met	Ala	Gly	Ile	Ala	Ala	Lys	Leu	Ala	Lys	Asp	Arg	Glu	Ala	Ala	Glu
1				5					10					15	
Gly	Leu	Gly	Ser	His	Glu	Arg	Ala	Ile	Lys	Tyr	Leu	Asn	Gln	Asp	Tyr
			20					25					30		
Glu	Ala	Leu	Arg	Asn	Glu	Cys	Leu	Glu	Ala	Gly	Thr	Leu	Phe	Gln	Asp
		35					40					45			
Pro	Ser	Phe	Pro	Ala	Ile	Pro	Ser	Ala	Leu	Gly	Phe	Lys	Glu	Leu	Gly
	50					55					60				
Pro	Tyr	Ser	Ser	Lys	Thr	Arg	Gly	Met	Arg	Trp	Lys	Arg	Pro	Thr	Glu
65					70					75					80
Ile	Cys	Ala	Asp	Pro	Gln	Phe	Ile	Ile	Gly	Gly	Ala	Thr	Arg	Thr	Asp
				85					90					95	
Ile	Cys	Gln	Gly	Ala	Leu	Gly	Asp	Cys	Trp	Leu	Leu	Ala	Ala	Ile	Ala
			100					105					110		
Ser	Leu	Thr	Leu	Asn	Glu	Glu	Ile	Leu	Ala	Arg	Val	Val	Pro	Leu	Asn
		115					120					125			
Gln	Ser	Phe	Gln	Glu	Asn	Tyr	Ala	Gly	Ile	Phe	His	Phe	Gln	Phe	Trp
	130					135					140				
Gln	Tyr	Gly	Glu	Trp	Val	Glu	Val	Val	Val	Asp	Asp	Arg	Leu	Pro	Thr
145					150					155					160
Lys	Asp	Gly	Glu	Leu	Leu	Phe	Val	His	Ser	Ala	Glu	Gly	Ser	Glu	Phe
				165					170					175	
Trp	Ser	Ala	Leu	Leu	Glu	Lys	Ala	Tyr	Ala	Lys	Ile	Asn	Gly	Cys	Tyr
			180					185					190		
Glu	Ala	Leu	Ser	Gly	Gly	Ala	Thr	Thr	Glu	Gly	Phe	Glu	Asp	Phe	Thr
		195					200					205			

Gly	Gly	Ile	Ala	Glu	Trp	Tyr	Glu	Leu	Lys	Lys	Pro	Pro	Pro	Asn	Leu
	210					215					220				
Phe	Lys	Ile	Ile	Gln	Lys	Ala	Leu	Gln	Lys	Gly	Ser	Leu	Leu	Gly	Cys
225					230					235					240
Ser	Ile	Asp	Ile	Thr	Ser	Ala	Ala	Asp	Ser	Glu	Ala	Ile	Thr	Phe	Gln
				245					250					255	
Lys	Leu	Val	Lys	Gly	His	Ala	Tyr	Ser	Val	Thr	Gly	Ala	Glu	Glu	Val
			260					265					270		
Glu	Ser	Asn	Gly	Ser	Leu	Gln	Lys	Leu	Ile	Arg	Ile	Arg	Asn	Pro	Trp
		275					280					285			
Gly	Glu	Val	Glu	Trp	Thr	Gly	Arg	Trp	Asn	Asp	Asn	Cys	Pro	Ser	Trp
	290					295					300				
Asn	Thr	Ile	Asp	Pro	Glu	Glu	Arg	Glu	Arg	Leu	Thr	Arg	Arg	His	Glu
305					310					315					320
Asp	Gly	Glu	Phe	Trp	Met	Ser	Phe	Ser	Asp	Phe	Leu	Arg	His	Tyr	Ser
				325					330					335	
Arg	Leu	Glu	Ile	Cys	Asn	Leu	Thr	Pro	Asp	Thr	Leu	Thr	Ser	Asp	Thr
			340					345					350		
Tyr	Lys	Lys	Trp	Lys	Leu	Thr	Lys	Met	Asp	Gly	Asn	Trp	Arg	Arg	Gly
		355					360					365			
Ser	Thr	Ala	Gly	Gly	Cys	Arg	Asn	Tyr	Pro	Asn	Thr	Phe	Trp	Met	Asn
	370					375					380				
Pro	Gln	Tyr	Leu	Ile	Lys	Leu	Glu	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Asp
385					390					395					400
Gly	Glu	Ser	Gly	Cys	Thr	Phe	Leu	Val	Gly	Leu	Ile	Gln	Lys	His	Arg
				405					410					415	
Arg	Arg	Gln	Arg	Lys	Met	Gly	Glu	Asp	Met	His	Thr	Ile	Gly	Phe	Gly
			420					425					430		
Ile	Tyr	Glu	Val	Pro	Glu	Glu	Leu	Ser	Gly	Gln	Thr	Asn	Ile	His	Leu
		435					440					445			
Ser	Lys	Asn	Phe	Phe	Leu	Thr	Asn	Arg	Ala	Arg	Glu	Arg	Ser	Asp	Thr
	450					455					460				
Phe	Ile	Asn	Leu	Arg	Glu	Val	Leu	Asn	Arg	Phe	Lys	Leu	Pro	Pro	Gly
465					470					475					480
Glu	Tyr	Ile	Leu	Val	Pro	Ser	Thr	Phe	Glu	Pro	Asn	Lys	Asp	Gly	Asp
				485					490					495	
Phe	Cys	Ile	Arg	Val	Phe	Ser	Glu	Lys	Lys	Ala	Asp	Tyr	Gln	Ala	Val
			500					505					510		
Asp	Asp	Glu	Ile	Glu	Ala	Asn	Leu	Glu	Glu	Phe	Asp	Ile	Ser	Glu	Asp
		515					520					525			
Asp	Ile	Asp	Asp	Gly	Val	Arg	Arg	Leu	Phe	Ala	Gln	Leu	Ala	Gly	Glu
	530					535					540				
Asp	Ala	Glu	Ile	Ser	Ala	Phe	Glu	Leu	Gln	Thr	Ile	Leu	Arg	Arg	Val
545					550					555					560

Leu Ala Lys Arg Gln Asp Ile Lys Ser Asp Gly Phe Ser Ile Glu Thr
 565 570 575
 Cys Lys Ile Met Val Asp Met Leu Asp Ser Asp Gly Ser Gly Lys Leu
 580 585 590
 Gly Leu Lys Glu Phe Tyr Ile Leu Trp Thr Lys Ile Gln Lys Tyr Gln
 595 600 605
 Lys Ile Tyr Arg Glu Ile Asp Val Asp Arg Ser Gly Thr Met Asn Ser
 610 615 620
 Tyr Glu Met Arg Lys Ala Leu Glu Glu Ala Gly Phe Lys Met Pro Cys
 625 630 635 640
 Gln Leu His Gln Val Ile Val Ala Arg Phe Ala Asp Asp Gln Leu Ile
 645 650 655
 Ile Asp Phe Asp Asn Phe Val Arg Cys Leu Val Arg Leu Glu Thr Leu
 660 665 670
 Phe Lys Ile Phe Lys Gln Leu Asp Pro Glu Asn Thr Gly Thr Ile Glu
 675 680 685
 Leu Asp Leu Ile Ser Trp Leu Cys Phe Ser Val Leu
 690 695 700